AMENDMENTS TO THE SPECIFICATION:

Please amend the paragraph at page 11, lines 13-17 as follows:

The CTS sequence of the EIAV lentivirus has recently been characterized (Scott R. Stetor et al Biochemistry 1999, 38, p 3656-67). According to the authors, in EIAV, the cPPT and CTS sequences are, respectively,

5'AAC AAA GGG AGG GA3' (SEQ ID NO: 1) and

5' AAA AAA TTT TGT TTT TAC AAA ATC 3' (SEQ ID NO: 2).

Please amend the paragraph at page 22, lines 9-15, of the specification as follows:

FIGS 11A-11F: Polynucleotide sequence comprising cPPT and CTS regions of the CAEV (SEQ ID NO: 9), **EIAV** (SEQ ID NO: 10), **VISNA** (SEQ ID NO: 11),**SIV_{AGM}** (SEQ ID NO: 12), **$HIV\text{-}2_{ROD}$** (SEQ ID NO: 13), **and $HIV\text{-}1_{LAI}$** (SEQ ID NO: 14) **viruses.**

FIG 11G: represents the triplex DNA sequence of the HIV-1 virus (SEQ ID NO: 33). The cis-acting regions, cPPT and CTS, are boxed and printed in bold capitals.

FIG 11H: represents the alignment of cPPT and 3' PPT sequences in several lentiviruses. The top line corresponds to the 3' PPT sequence present in all retroviruses upstream of 3' LTR HIV-1 (SEQ ID NO: 15); HIV-2 ROD (SEQ ID NO: 16); SIVmac and HIV-2 NIH-Z (SEQ ID NO: 17); SIVagm (SEQ ID NO: 18); VISNA (SEQ ID NO: 19); CAEV (SEQ ID NO: 20); EIAV (SEQ ID NO: 21). The bottom line corresponds to the internal repetition of the PPT sequence termed the cPPT in the lentivirus.

Please amend that paragraph at page 23, lines 3-4, as follows:

FIG 15: Sequences for specific CT1 HLA A2.1 melanoma epitopes included in the polyepitopic construction of the pTRIP.MEL-IRES-GFP vector. gp100 154-162 (SEQ ID NO: 22), gp 100 209-217 (SEQ ID NO: 23), gp 100 280-288 (SEQ ID NO: 24), gp 100 457-466 (SEQ ID NO: 25); MART-1 27-35 (SEQ ID NO: 26), MART-1 32-40 (SEQ ID NO: 27); TYROSINASE 1-9 (SEQ ID NO: 28), TYROSINASE 368-376-D (SEQ ID NO: 29); Gnt-V/NA17-A nt38-64[b] (SEQ ID NO: 30) MAGE-3 271-279 (SEQ ID NO: 31); amino acid sequence of melanoma polyepitope (SEQ ID NO: 32). The sequences of the polyepitope are underlined to distinguish each epitope.

Please amend the paragraph at page 23, lines 18-20, as follows:

The sequences for the PCR primers used were as follows:

Bam EGFP: 5' cc gga tcc cca ccg gtc gcc acc 3' (SEQ ID NO: 3)

Xho EGP: 5' cc ctc gag cta gag tcg cgg ccg 3' (SEQ ID NO: 4).

Please amend the paragraph at page 24, lines 13-15, as follows:

The sequences for the PCR primers were as follows:

Nar/Eco TRIP+: 5' gtc gtc ggc gcc gaa ttc aca aat ggc agt att cat cc 3' (SEQ ID NO: 5)

Nar TRIP-: 5' gtc gtc ggc gcc cca aag tgg atc tct gct gtc c 3' (SEQ ID NO: 6).

Please amend the paragraph at page 39, lines 4-14, as follows:

Firstly, a bicistronic TRIP-IRES-GFP vector was constructed. The EcoRI site of the TRIP-IRES-GFP vector was filled with T4 DNA polymerase creating the TRIP-

deltaE-GFP vector. Then a fragment of about 1.2 kb, BamHI-BstXI-SnaBI-EcoRI-IRES-EGFP-XhoI, was cloned in the place of the BamHI-EGFP-XhoI fragment. The fragment containing the IRES-EGFP (internal ribosome entry site) was generously donated by Dr. Yongwhon Choi (Rockefeller University, NY, USA). A fragment containing a Kozac consensus sequence and a melanoma CTL polyepitope was generated by PCR, using the pBS mel poly matrix with pfu polymerase and the following oligonucleotides: 5BglmIu Mel: 5' cc aga tct acg cgt gcc acc atg gct gct ggt 3' (SEQ ID NO: 7); 3RIMeI: 5' CG GAA TTC GAC CTA AAC GCA ACG GAT G 3' (SEQ ID NO: 8). The mel PCR fragment was then digested with BglII and EcoRI and cloned to the BamHI and EcoRI sites of the TRIP-deltaE-IRES-GFP vector creating the TRIP-MEL-IRES-GFP vector.